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```
{r load_pander_methods,results='hide'} require(pander) replace.print.methods
<- function(PKG_name = "pander") { PKG_methods <- as.character(methods(PKG_name))
print_methods <- gsub(PKG_name, "print", PKG_methods) for(i in
seq_along(PKG_methods)) { f <- eval(parse(text=paste(PKG_name,":::",
PKG_methods[i], sep = ""))) # the new function to use for print
assign(print_methods[i], f, ".GlobalEnv") } } replace.print.methods()
## The following might work with some tweaks:  ## print <- function
(x, ...)  UseMethod("pander")
```

Introduction

The dataMineR script toolbox aims to be a efficient set of R & knitr scripts, that can be used by experienced and less experience dataminers. The toolbox uses the best of the R community to efficently analayse any arbritray dataset and make a predictive model on the target variable. The toolbox uses R `version$version.string`}, R-studio and knitr(http://yihui.name/knitr/) to knit R code and Latex into nice and readable pdf reports. We have the option to include all R code that is used to generate the plots and calculations (see "chunk_options"). By default this feauture is dissabled.

CRoss Industry Standard Process for datamining

In this toolkit we will use the CRISP methodology to guide the datamining proces.

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Some text explaining the analysis we are doing

```
{r comment = NA, results = 'asis'} lm(mpg ~ wt, data = mtcars)
summary(cars)# a summary table fit <- lm(dist~speed, data = cars)
fit plot(cars) # a plot
```

This report was generated with R (2.15.2) and pander (0.3.1) on x86_64-apple-darwin9.8.0 platform.